

## Fig.1a-1

### Nucleic acid and amino acid sequence of TTXi DRG sodium channel

```
tagcttgcttctgctaattgctaccccaggccttttagacagagaacagatggcagatggag
1 -----+-----+-----+-----+-----+-----+-----+
atcgaacgaagacgattacgatgggggtccggaaatctgtctcttgtctaccgtctacctc

tttcttattgccaatgcgcaaacgctgagccacctcatgatcccggaccccatgggttttc
61 -----+-----+-----+-----+-----+-----+-----+
aaagaataacggtacgcgtttgcgactcgggtggagtactagggcctgggggtaccaaag

agtagacaacctgggctaagaagagatctccgaccttatagagcagcaaagagtgtaaat
121 -----+-----+-----+-----+-----+-----+-----+
tcattctgttggaacccgattcttctcttagaggctggaatatctcgtcgtttctcacattta

tcttcccccaagaagaatgagaagATGGAGCTCCCCTTTGCGTCCGTGGGAACCTACCAATT
181 -----+-----+-----+-----+-----+-----+-----+
agaaggggttcttcttactcttcTACCTCGAGGGGAAACGCAGGCACCCTTGATGGTTAA

M E L P F A S V G T T N F

TCAGACGGTTCCTCCAGAGTCACTGGCAGAGATCGAGAAGCAGATTGCTGCTCACC GGG
241 -----+-----+-----+-----+-----+-----+-----+
AGTCTGCCAAGTGAGGTCTCAGTGACCGTCTCTAGCTCTTCGTCTAACGACGAGTG GCCC

R R F T P E S L A E I E K Q I A A H R A

CAGCCAAGAAGGCCAGAACCAAGCACAGAGGACAGGAGGACAAGGGCGAGAAGCCCAGGC
301 -----+-----+-----+-----+-----+-----+-----+
GTCGGTTCTTCCGGTCTTGGTTCGTGTCTCCTGTCCTCCTGTTCCCGCTCTTCGGGTCCG

A K K A R T K H R G Q E D K G E K P R P

CTCAGCTGGACTTGAAAGACTGTAACCAGCTGCCCAAGTTCTATGGTGAGCTCCCAGCAG
361 -----+-----+-----+-----+-----+-----+-----+
GAGTCGACCTGAACTTTCTGACATTGGTCGACGGGTTCAGATACCACTCGAGGGTCGTC

Q L D L K D C N Q L P K F Y G E L P A E

AACTGGTCGGGGAGCCCCCTGGAGGACCTAGACCCTTTCTACAGCACACACCGGACATTCA
421 -----+-----+-----+-----+-----+-----+-----+
TTGACCAGCCCCCTCGGGGACCTCCTGGATCTGGGAAAGATGTCGTGTGTGGCCTGTAAGT

L V G E P L E D L D P F Y S T H R T F M

TGGTGTGTAATAAAAGCAGGACCATTTCCAGATTCAAGTGCCACTTGGGCCCTGTGGCTCT
481 -----+-----+-----+-----+-----+-----+-----+
ACCACAACCTTATTTTCGTCCTGGTAAAGGTCTAAGTCACGGTGAACCCGGGACACCGAGA

V L N K S R T I S R F S A T W A L W L F
```

## Fig.1a-2

TCAGTCCCTTCAACCTGATCAGAAGAACAGCCATCAAAGTGTCTGTCCATTCTGGTTCT  
541 -----+-----+-----+-----+-----+-----+-----+  
AGTCAGGGAAGTTGGACTAGTCTTCTTGTGCGTAGTTTCACAGACAGGTAAGGACCAAGA  
S P F N L I R R T A I K V S V H S W F S  
CCATATTTCATCACCATCACTATTTTGGTCAACTGCGTGTGCATGACCCGAACTGATCTTC  
601 -----+-----+-----+-----+-----+-----+-----+  
GGTATAAGTAGTGGTAGTGATAAAACCAGTTGACGCACACGTAAGTGGGCTTGACTAGAAG  
I F I T I T I L V N C V C M T R T D L P  
CAGAGAAAGTCGAGTACGTCTTCACTGTCAATTTACACCTTCGAGGCTCTGATTAAGATAC  
661 -----+-----+-----+-----+-----+-----+-----+  
GTCTCTTTCAGCTCATGCAGAAGTGACAGTAAATGTGGAAGCTCCGAGACTAATTCTATG  
E K V E Y V F T V I Y T F E A L I K I L  
TGGCAAGAGGGTTTTGTCTAAATGAGTTCACTTATCTTCGAGATCCGTGGAAGTGGCTGG  
721 -----+-----+-----+-----+-----+-----+-----+  
ACCGTTCTCCCAAACAGATTTACTCAAGTGAATAGAAGCTCTAGGCACCTTGACCGACC  
A R G F C L N E F T Y L R D P W N W L D  
ACTTCAGTGTCAATTACCTTGGCGTATGTGGGTGCAGCGATAGACCTCCGAGGAATCTCAG  
781 -----+-----+-----+-----+-----+-----+-----+  
TGAAGTCACAGTAATGGAACCGCATAACCCACGTCGCTATCTGGAGGCTCCTTAGAGTC  
F S V I T L A Y V G A A I D L R G I S G -  
GCCTGCGGACATTCCGAGTTCTCAGAGCCCTGAAAAGTGTCTGTGATCCAGGACTGA  
841 -----+-----+-----+-----+-----+-----+-----+  
CGGACGCCTGTAAGGCTCAAGAGTCTCGGGACTTTTGACAAAGACACTAGGGTCTGACT  
L R T F R V L R A L K T V S V I P G L K -  
AGGTCATCGTGGGAGCCCTGATCCACTCAGTGAGGAAGCTGGCCGACGTGACTATCCTCA  
901 -----+-----+-----+-----+-----+-----+-----+  
TCCAGTAGCACCCCTCGGGACTAGGTGAGTCACTCCTTCGACCGGCTGCACTGATAGGAGT  
V I V G A L I H S V R K L A D V T I L T  
CAGTCTTCTGCCTGAGCGTCTTCGCCTTGGTGGGCCTGCAGCTCTTTAAGGGGAACCTTA  
961 -----+-----+-----+-----+-----+-----+-----+  
GTCAGAAGACGGACTCGCAGAAGCGGAACCAACCGGACGTCGAGAAATTCCCCTTGGAAT  
V F C L S V F A L V G L Q L F K G N L K  
AGAACAAATGCATCAGGAACGGAACAGATCCCCACAAGGCTGACAACCTCTCATCTGAAA  
1021 -----+-----+-----+-----+-----+-----+-----+  
TCTTGTTTACGTAGTCCTTGCCTTGTCTAGGGGTGTTCCGACTGTTGGAGAGTAGACTTT  
N K C I R N G T D P H K A D N L S S E M  
TGGCAGAATACATCTTCATCAAGCCTGGTACTACGGATCCCTTACTGTGCGGCAATGGGT  
1081 -----+-----+-----+-----+-----+-----+-----+  
ACCGTCTTATGTAGAAGTAGTTCCGACCATGATGCCTAGGGAATGACACGCCGTTACCCA  
A E Y I F I K P G T T D P L L C G N G S

## Fig.1a-3

1141 CTGATGCTGGTCACTGCCCTGGAGGCTATGTCTGCCTGAAAACCTCCTGACAACCCGGATT  
-----+-----+-----+-----+-----+-----+-----+  
GACTACGACCAGTGACGGGACCTCCGATACAGACGGACTTTTGAGGACTGTTGGGCCTAA  
D A G H C P G G Y V C L K T P D N P D F  
1201 TTA ACTACACCAGCTTTGATTCCCTTTGCGTGGGCATTCCCTCTCACTGTTCCGCCTCATGA  
-----+-----+-----+-----+-----+-----+-----+  
AATTGATGTGGTCGAAACTAAGGAAACGCACCCGTAAGGAGAGTGACAAGGCGGAGTACT  
N Y T S F D S F A W A F L S L F R L M T  
1261 CGCAGGACTCCTGGGAGCGCCTGTACCAGCAGACACTCCGGGCTTCTGGGAAAATGTACA  
-----+-----+-----+-----+-----+-----+-----+  
GCGTCCTGAGGACCCTCGCGGACATGGTCGTCTGTGAGGCCCGAAGACCCTTTTACATGT  
Q D S W E R L Y Q Q T L R A S G K M Y M  
1321 TGGTCTTTTTTCGTGCTGGTTATTTTCCTTGATCGTTCTACCTGGTCAATTTGATCTTGG  
-----+-----+-----+-----+-----+-----+-----+  
ACCAGAAAAAGCACGACCAATAAAAGGAACCTAGCAAGATGGACCAGTTAACTAGAAC  
V F F V L V I F L G S F Y L V N L I L A  
1381 CCGTGGTCACCATGGCGTATGAAGAGCAGAGCCAGGCAACAATTGCAGAAATCGAAGCCA  
-----+-----+-----+-----+-----+-----+-----+  
GGCACCAGTGGTACCGCATACTTCTCGTCTCGGTCCGTTGTTAACGTCTTTAGCTTCGGT  
V V T M A Y E E Q S Q A T I A E I E A K  
1441 AGGAAAAAAAGTTCCAGGAAGCCCTTGAGGTGCTGCAGAAGGAACAGGAGGTGCTGGCAG  
-----+-----+-----+-----+-----+-----+-----+  
TCCTTTTTTTCAAGGTCTTCGGGAACCTCCACGACGTCTTCCTTGTCCTCCACGACCGTC  
E K K F Q E A L E V L Q K E Q E V L A A  
1501 CCCTGGGGATTGACACGACCTCGCTCCAGTCCCACAGTGGATCACCTTAGCCTCCAAAA  
-----+-----+-----+-----+-----+-----+-----+  
GGGACCCCTAACTGTGCTGGAGCGAGGTGAGGGTGTACCTAGTGGGAATCGGAGGTTTT  
L G I D T T S L Q S H S G S P L A S K N  
1561 ACGCCAATGAGAGAAGACCCAGGGTGAAATCAAGGGTGTGAGAGGGCTCCACGGATGACA  
-----+-----+-----+-----+-----+-----+-----+  
TGCGGTTACTCTCTTCTGGGTCCCACTTTAGTTCCACAGTCTCCCGAGGTGCCTACTGT  
A N E R R P R V K S R V S E G S T D D N  
1621 ACAGGTCACCCCAATCTGACCCTTACAACCAGCGCAGGATGTCTTTCCTAGGCCTGTCTT  
-----+-----+-----+-----+-----+-----+-----+  
TGTCCAGTGGGGTTAGACTGGGAATGTTGGTCGCGTCCTACAGAAAGGATCCGGACAGAA  
R S P Q S D P Y N Q R R M S F L G L S S  
1681 CAGGAAGACGCAGGGCTAGCCACGGCAGTGTGTTCCACTTCCGAGCGCCCAGCCAAGACA  
-----+-----+-----+-----+-----+-----+-----+  
GTCCTTCTGCGTCCCGATCGGTGCCGTACACAAGGTGAAGGCTCGCGGGTTCGGTTCTGT  
G R R R A S H G S V F H F R A P S Q D I

## Fig.1a-4

1741 TCTCATTTCCTGACGGGATCACCCCTGATGATGGGGTCTTTCACGGAGACCAGGAAAGCC  
-----+-----+-----+-----+-----+-----+-----+  
AGAGTAAAGGACTGCCCTAGTGGGGACTACTACCCAGAAAGTGCCTCTGGTCCTTTTCGG  
S F P D G I T P D D G V F H G D Q E S R  
GTCGAGGTTCCATATTGCTGGGCAGGGGTGCTGGGCAGACAGGTCCACTCCCCAGGAGCC  
1801 -----+-----+-----+-----+-----+-----+-----+  
CAGCTCCAAGGTATAACGACCCGTCCCCACGACCCGTCTGTCCAGGTGAGGGGTCTCTCG  
R G S I L L G R G A G Q T G P L P R S P  
CACTGCCTCAGTCCCCCAACCCTGGCCGTAGACATGGAGAAGAGGGACAGCTCGGAGTGC  
1861 -----+-----+-----+-----+-----+-----+-----+  
GTGACGGAGTCAGGGGGTTGGGACCGGCATCTGTACCTCTTCTCCCTGTCGAGCCTCACG  
L P Q S P N P G R R H G E E G Q L G V P  
CCACTGGTGAGCTTACCGCTGGAGCGCCTGAAGGCCCGGCACTCGACACTACAGGGCAGA  
1921 -----+-----+-----+-----+-----+-----+-----+  
GGTGACCACTCGAATGGCGACCTCGCGGACTTCCGGGCCGTGAGCTGTGATGTCCCGTCT  
T G E L T A G A P E G P A L D T T G Q K  
AGAGCTTCCTGTCTGCGGGCTACTTGAACGAACCTTTCCGAGCACAGAGGGCCATGAGCG  
1981 -----+-----+-----+-----+-----+-----+-----+  
TCTCGAAGGACAGACGCCCGATGAACTTGCTTGGAAAGGCTCGTGTCTCCCGGTACTCG  
S F L S A G Y L N E P F R A Q R A M S V  
TTGTCAGTATCATGACTTCTGTCAATTGAGGAGCTTGAAGAGTCTAAGCTGAAGTGCCAC  
2041 -----+-----+-----+-----+-----+-----+-----+  
AACAGTCATAGTACTGAAGACAGTAACTCCTCGAACTTCTCAGATTCGACTTCACGGGTG  
V S I M T S V I E E L E E S K L K C P P  
CCTGCTTGATCAGCTTCGCTCAGAAGTATCTGATCTGGGAGTGCTGCCCCAAGTGGAGGA  
2101 -----+-----+-----+-----+-----+-----+-----+  
GGACGAACTAGTCGAAGCGAGTCTTCATAGACTAGACCCTCACGACGGGGTTACCTCCT  
C L I S F A Q K Y L I W E C C P K W R K  
AGTTCAAGATGGCGCTGTTCGAGCTGGTGACTGACCCCTTCGCAGAGCTTACCATCACCC  
2161 -----+-----+-----+-----+-----+-----+-----+  
TCAAGTTCTACCGCGACAAGCTCGACCACTGACTGGGGAAGCGTCTCGAATGGTAGTGGG  
F K M A L F E L V T D P F A E L T I T L  
TCTGCATCGTGGTGAACACCGTCTTCATGGCCATGGAGCACTACCCCATGACCGATGCCT  
2221 -----+-----+-----+-----+-----+-----+-----+  
AGACGTAGCACCCTTGTGGCAGAAGTACCGGTACCTCGTGTGAGGGTACTGGCTACGGA  
C I V V N T V F M A M E H Y P M T D A F  
TCGATGCCATGCTTCAAGCCGGCAACATTGTCTTCACCGTGTTCACCAATGGAGATGG  
2281 -----+-----+-----+-----+-----+-----+-----+  
AGCTACGGTACGAAGTTCGGCCGTTGTAACAGAAGTGGCACAAAAGTGTTACCTCTACC  
D A M L Q A G N I V F T V F F T M E M A

## Fig.1a-5

2341 CCTTCAAGATCATTGCCTTCGACCCCTACTATTACTTCCAGAAGAAGTGAATATCTTCG  
-----+-----+-----+-----+-----+  
GGAAGTTCTAGTAACGGAAGCTGGGGATGATAATGAAGGTCTTCTTCACCTTATAGAAGC  
F K I I A F D P Y Y Y F Q K K W N I F D  
2401 ACTGTGTCATCGTCACCGTGAGCCTTCTGGAGCTGAGTGCATCCAAGAAGGGCAGCCTGT  
-----+-----+-----+-----+-----+  
TGACACAGTAGCAGTGGCACTCGGAAGACCTCGACTCACGTAGGTTCTTCCCGTCGGACA  
C V I V T V S L L E L S A S K K G S L S  
2461 CTGTGCTCCGTTCTTACGCTTGCTGCGGGTCTTCAAGCTGGCCAAGTCTTGGCCCCACCC  
-----+-----+-----+-----+-----+  
GACACGAGGCAAGGAATGCGAACGACGCCCAGAAGTTCGACCGGTTACAGACCGGGTGGG  
V L R S L R L L R V F K L A K S W P T L  
2521 TGAACACCCTCATCAAGATCATCGGGAAGTCAAGTGGGGGCCCTGGGCAACCTGACCTTTA  
-----+-----+-----+-----+-----+  
ACTTGTGGGAGTAGTTCTAGTAGCCCTTGAGTCACCCCGGGACCCGTTGGACTGGAAT  
N T L I K I I G N S V G A L G N L T F I  
2581 TCCTGGCCATCATCGTCTTCATCTTCGCCCTGGTTCGGAAAGCAGCTTCTCTCAGAGGACT  
-----+-----+-----+-----+-----+  
AGGACCGGTAGTAGCAGAAGTAGAAGCGGGACCAGCCTTTCGTCGAAGAGAGTCTCCTGA  
L A I I V F I F A L V G K Q L L S E D Y  
2641 ACGGGTGCCGCAAGGACGGCGTCTCCGTGTGGAACGGCGAGAAGCTCCGCTGGCACATGT  
-----+-----+-----+-----+-----+  
TGCCACGCGGCTTCTGCGCAGAGGCACACCTTGCCGCTCTTCGAGGCGACCGTGTACA  
G C R K D G V S V W N G E K L R W H M C  
2701 GTGACTTCTTCCATTCCCTTCCTGGTCTTCCGAATCCTCTGCGGGGAGTGGATCGAGA  
-----+-----+-----+-----+-----+  
CACTGAAGAAGGTAAGGAAGGACCAGCAGAAGGCTTAGGAGACGCCCTCACCTAGCTCT  
D F F H S F L V V F R I L C G E W I E N  
2761 ACATGTGGGTCTGCATGGAGGTCAGCCAGAAATCCATCTGCCTCATCCTCTTCTTGACTG  
-----+-----+-----+-----+-----+  
TGTACACCCAGACGTACCTCCAGTCGGTCTTTAGGTAGACGGAGTAGGAGAAGAACTGAC  
M W V C M E V S Q K S I C L I L F L T V  
2821 TGATGGTGTCTGGGCAACCTAGTGGTGTCTCAACCTTTTCATCGCTTTACTGCTGAACTCCT  
-----+-----+-----+-----+-----+  
ACTACCACGACCCGTTGGATCACCACGAGTTGGAAGAGTAGCGAAATGACGACTTGAGGA  
M V L G N L V V L N L F I A L L L N S F  
2881 TCAGCGCGGACAACCTCACGGCTCCAGAGGATGACGGGGAGGTGAACAACTTGACAGTTAG  
-----+-----+-----+-----+-----+  
AGTCGCGCCTGTTGGAGTGCCGAGGTCTCCTACTGCCCTCCACTTGTTGAACGTCAATC  
S A D N L T A P E D D G E V N N L Q L A

## Fig.1a-6

2941 CACTGGCCAGGATCCAGGTACTTGGCCATCGGGCCAGCAGGGCCATCGCCAGTTACATCA  
-----+-----+-----+-----+-----+-----+-----+  
GTGACCGGTCCTAGGTCCATGAACCGGTAGCCCGGTCTGTCCTCCGGTAGCGGTCAATGTAGT  
L A R I Q V L G H R A S R A I A S Y I S  
3001 GCAGCCACTGCCGATTCCGCTGGCCCAAGGTGGAGACCCAGCTGGGCATGAAGCCCCCAC  
-----+-----+-----+-----+-----+-----+-----+  
CGTCGGTGACGGCTAAGGCGACCGGGTTCCACCTCTGGGTCTGACCCGTACTTCGGGGGGTG  
S H C R F R W P K V E T Q L G M K P P L  
3061 TCACCAGCTCAGAGGCCAAGAACCACATTGCCACTGATGCTGTCAGTGCTGCAGTGGGGA  
-----+-----+-----+-----+-----+-----+-----+  
AGTGGTCGAGTCTCCGGTTCTTGGTGTAACGGTGACTACGACAGTCACGACGTCACCCCT  
T S S E A K N H I A T D A V S A A V G N  
3121 ACCTGACAAAGCCAGCTCTCAGTAGCCCCAAGGAGAATCACGGGGACTTCATCACTGATC  
-----+-----+-----+-----+-----+-----+-----+  
TGGACTGTTTCGGTCGAGAGTCATCGGGGTTCTCTTAGTGCCCCTGAAGTAGTGACTAG  
L T K P A L S S P K E N H G D F I T D P  
3181 CCAACGTGTGGGTCTCTGTGCCCATTTGCTGAGGGGGAATCTGACCTCGACGAGCTCGAGG  
-----+-----+-----+-----+-----+-----+-----+  
GGTTGCACACCCAGAGACACGGGTAACGACTCCCCCTTAGACTGGAGCTGCTCGAGCTCC  
N V W V S V P I A E G E S D L D E L E E  
3241 AAGATATGGAGCAGGCTTCGCAGAGCTCCTGGCAGGAAGAGGACCCCAAGGGACAGCAGG  
-----+-----+-----+-----+-----+-----+-----+  
TTCTATACCTCGTCCGAAGCGTCTCGAGGACCGTCTTCTCCTGGGGTTCCCTGTCTGCTCC  
D M E Q A S Q S S W Q E E D P K G Q Q E  
3301 AGCAGTTGCCACAAGTCCAAAAGTGTGAAAACCACCAGGCAGCCAGAAGCCCAGCCTCCA  
-----+-----+-----+-----+-----+-----+-----+  
TCGTCAACGGTGTTTCAGGTTTTACACTTTTGGTGGTCCGTCGGTCTTCGGGTCTGGAGGT  
Q L P Q V Q K C E N H Q A A R S P A S M  
3361 TGATGTCCTCTGAGGACCTGGCTCCATACCTGGGTGAGAGCTGGAAGAGGAAGGATAGCC  
-----+-----+-----+-----+-----+-----+-----+  
ACTACAGGAGACTCCTGGACCGAGGTATGGACCCACTCTCGACCTTCTCCTTCCTATCGG  
M S S E D L A P Y L G E S W K R K D S P  
3421 CTCAGGTCCCTGCCGAGGGAGTGGATGACACGAGCTCCTCTGAGGGCAGCACGGTGGACT  
-----+-----+-----+-----+-----+-----+-----+  
GAGTCCAGGGACGGCTCCCTCACCTACTGTGCTCGAGGAGACTCCCGTCGTGCCACCTGA  
Q V P A E G V D D T S S S E G S T V D C  
3481 GCCCGGACCCAGAGGAAATCCTGAGGAAGATCCCCGAGCTGGCAGATGACCTGGACGAGC  
-----+-----+-----+-----+-----+-----+-----+  
CGGGCCTGGGTCTCCTTTAGGACTCCTTCTAGGGGCTCGACCGTCTACTGGACCTGCTCG  
P D P E E I L R K I P E L A D D L D E P

## Fig. 1a-7

3541 CCGATGACTGTTTCACAGAAGGCTGCACTCGCCGCTGTCCCTGCTGCAACGTGAATACTA  
-----+-----+-----+-----+-----+-----+-----+  
GGCTACTGACAAAGTGTCTTCCGACGTGAGCGGCGACAGGGACGACGTTGCACTTATGAT  
D D C F T E G C T R R C P C C N V N T S  
3601 GCAAGTCTCCTTGGGCCACAGGCTGGCAGGTGCGCAAGACCTGCTACCGCATCGTGGAGC  
-----+-----+-----+-----+-----+-----+-----+  
CGTTCAGAGGAACCCGGTGTCCGACCGTCCACGCGTTCTGGACGATGGCGTAGCACCTCG  
K S P W A T G W Q V R K T C Y R I V E H  
3661 ACAGCTGGTTTGAGAGTTTCATCATCTTCATGATCCTGCTCAGCAGTGGAGCGCTGGCCT  
-----+-----+-----+-----+-----+-----+-----+  
TGTCGACCAAACCTCTCAAAGTAGTAGAAGTACTAGGACGAGTCGTCACCTCGCGACCGGA  
S W F E S F I I F M I L L S S G A L A F  
3721 TTGAGGATAACTACCTGGAAGAGAAACCCCGAGTGAAGTCCGTGCTGGAGTACACTGACC  
-----+-----+-----+-----+-----+-----+-----+  
AACTCCTATTGATGGACCTTCTCTTTGGGGCTCACTTCAGGCACGACCTCATGTGACTGG  
E D N Y L E E K P R V K S V L E Y T D R  
3781 GAGTGTTACACCTTCATCTTCGTCTTTGAGATGCTGCTCAAGTGGGTAGCCTATGGCTTCA  
-----+-----+-----+-----+-----+-----+-----+  
CTCACAAGTGGAGTAGAAGCAGAACTCTACGACGAGTTCACCCATCGGATACCGAAGT  
V F T F I F V F E M L L K W V A Y G F K  
3841 AAAAGTATTTACCAATGCCTGGTGCTGGCTGGACTTCCTCATTGTGAACATCTCCCTGA  
-----+-----+-----+-----+-----+-----+-----+  
TTTTCATAAAGTGGTTACGGACCACGACCGACCTGAAGGAGTAACACTTGTAGAGGGACT  
K Y F T N A W C W L D F L I V N I S L T  
3901 CAAGCCTCATAGCGAAGATCCTTGAGTATTCCGACGTGGCGTCCATCAAAGCCCTTCGGA  
-----+-----+-----+-----+-----+-----+-----+  
GTTCCGAGTATCGCTTCTAGGAACTCATAAGGCTGCACCGCAGGTAGTTTCGGAAGCCT  
S L I A K I L E Y S D V A S I K A L R T  
3961 CTCTCCGTGCCCTCCGACCGCTGCGGGCTCTGTCTCGATTCTGAAGGCATGAGGGTAGTGG  
-----+-----+-----+-----+-----+-----+-----+  
GAGAGGCACGGGAGGCTGGCGACGCCCCGAGACAGAGCTAAGCTTCCGTACTCCCATCACC  
L R A L R P L R A L S R F E G M R V V V  
4021 TGGATGCCCTCGTGGGCGCCATCCCCCTCCATCATGAACGTCCTCCTCGTCTGCCTCATCT  
-----+-----+-----+-----+-----+-----+-----+  
ACCTACGGGAGCACCCGCGGTAGGGGAGGTAGTACTTGCAGGAGGAGCAGACGGAGTAGA  
D A L V G A I P S I M N V L L V C L I F  
4081 TCTGGCTCATCTTCAGCATCATGGGCGTGAACCTCTTCGCCGGGAAATTTTCGAAGTGCG  
-----+-----+-----+-----+-----+-----+-----+  
AGACCGAGTAGAAGTCGTAGTACCCGCACTTGAGAGAAGCGGCCCTTTAAAGCTTCACGC  
W L I F S I M G V N L F A G K F S K C V

## Fig. 1a-8

4141 TCGACACCAGAAATAACCCATTTTCCAACGTGAATTCGACGATGGTGAATAACAAGTCCG  
-----+-----+-----+-----+-----+-----+-----+  
AGCTGTGGTCTTTATTGGGTAAAAGGTTGCACTTAAGCTGCTACCACTTATTGTTTCAGGC  
D T R N N P F S N V N S T M V N N K S E  
AGTGTCAACAATCAAAACAGCACCGGCCACTTCTTCTGGGTCAACGTCAAAGTCAACTTCG  
4201 -----+-----+-----+-----+-----+-----+-----+  
TCACAGTGTTAGTTTTGTCTGCGGCCGGTGAAGAAGACCCAGTTGCAGTTTCAGTTGAAGC  
C H N Q N S T G H F F W V N V K V N F D  
ACAACGTCGCTATGGGCTACCTCGCACTTCTTCAGGTGGCAACCTTCAAAGGCTGGATGG  
4261 -----+-----+-----+-----+-----+-----+-----+  
TGTTGCAGCGATACCCGATGGAGCGTGAAGAAGTCCACCGTTGGAAGTTTCCGACCTACC  
N V A M G Y L A L L Q V A T F K G W M D  
ACATAATGTATGCAGCTGTTGATTCCGGAGAGATCAACAGTCAGCCTAACTGGGAGAACA  
4321 -----+-----+-----+-----+-----+-----+-----+  
TGTATTACATACGTCGACAACCTAAGGCCTCTCTAGTTGTCAGTCGGATTGACCTCTTGT  
I M Y A A V D S G E I N S Q P N W E N N  
ACTTGTACATGTACCTGTACTTCGTCGTTTTTCATCATTTTTCGGTGGCTTCTTCACGCTGA  
4381 -----+-----+-----+-----+-----+-----+-----+  
TGAACATGTACATGGACATGAAGCAGCAAAAGTAGTAAAAGCCACCGAAGAAGTGC GACT  
L Y M Y L Y F V V F I I F G G F F T L N  
ATCTCTTTGTTGGGGTCATAATCGACAACCTTCAACCAACAGAAAAAAAGCTAGGAGGCC  
4441 -----+-----+-----+-----+-----+-----+-----+  
TAGAGAAACAACCCAGTATTAGCTGTTGAAGTTGGTTGTCTTTTTTTTCGATCCTCCGG  
L F V G V I I D N F N Q Q K K K L G G Q  
AGGACATCTTCATGACAGAAGAGCAGAAGAAGTACTACAATGCCATGAAGAAGCTGGGCT  
4501 -----+-----+-----+-----+-----+-----+-----+  
TCCTGTAGAAGTACTGTCTTCTCGTCTTCTTCATGATGTTACGGTACTTCTTCGACCCGA  
D I F M T E E Q K K Y Y N A M K K L G S  
CCAAGAAACCCAGAACCCCATCCACGGCCCCTGAATAAGTACCAAGGCTTCGTGTTTG  
4561 -----+-----+-----+-----+-----+-----+-----+  
GGTTCTTTGGGGTCTTCGGGTAGGGTGCCGGGGACTTATTCATGGTTCCGAAGCACAAC  
K K P Q K P I P R P L N K Y Q G F V F D  
ACATCGTGACCAGGCAAGCCTTTGACATCATCATGTTCTCATCTGCCTCAACATGA  
4621 -----+-----+-----+-----+-----+-----+-----+  
TGTAGCACTGGTCCGTTTCGGAACTGTAGTAGTAGTACCAAGAGTAGACGGAGTTGTACT  
I V T R Q A F D I I I M V L I C L N M I  
TCACCATGATGGTGGAGACCGACGAGCAGGGCGAGGAGAAGACGAAGGTTCTGGGCAGAA  
4681 -----+-----+-----+-----+-----+-----+-----+  
AGTGGTACTACCACCTCTGGCTGCTCGTCCCGCTCCTCTTCTGCTTCCAAGACCCGTCTT  
T M M V E T D E Q G E E K T K V L G R I



## Fig. 1a-9

4741 TCAACCAGTTCTTTGTGGCCGTCTTCACGGGCGAGTGTGTGATGAAGATGTTCCGCCCTGC  
-----+-----+-----+-----+-----+-----+-----+  
AGTTGGTCAAGAAACACCGGCAGAAAGTGCCCGCTCACACACTACTTCTACAAGCGGGACG  
N Q F F V A V F T G E C V M K M F A L R  
GACAGTACTACTTCACCAACGGCTGGAACGTGTTTCGACTTCATAGTGGTGATCCTGTCCA  
4801 -----+-----+-----+-----+-----+-----+-----+  
CTGTCATGATGAAGTGGTTGCCGACCTTGACACAAGCTGAAGTATCACCACCTAGGACAGGT  
Q Y Y F T N G W N V F D F I V V I L S I  
TTGGGAGTCTGCTGTTTCTGCAATCCTTAAGTCACTGGAAAACACTTCTCCCCGACGC  
4861 -----+-----+-----+-----+-----+-----+-----+  
AACCCTCAGACGACAAAAGACGTTAGGAATTCAGTGACCTTTTGATGAAGAGGGGCTGCG  
G S L L F S A I L K S L E N Y F S P T L  
TCTTCCGGGTCATCCGTCTGGCCAGGATCGGCCGCATCCTCAGGCTGATCCGAGCAGCCA  
4921 -----+-----+-----+-----+-----+-----+-----+  
AGAAGGCCCAGTAGGCAGACCGGTCCTAGCCGGCGTAGGAGTCCGACTAGGCTCGTCGGT  
F R V I R L A R I G R I L R L I R A A K  
AGGGGATTCGCACGCTGCTCTTCGCCCTCATGATGTCCCTGCCCCGCCCTCTTCAACATCG  
4981 -----+-----+-----+-----+-----+-----+-----+  
TCCCCTAAGCGTGCGACGAGAAGCGGGAGTACTACAGGGACGGGCGGGAGAAGTTGTAGC  
G I R T L L F A L M M S L P A L F N I G  
GCCTCCTCCTCTTCCTCGTCATGTTTCATCTACTCCATCTTCGGCATGGCCAGCTTCGCTA  
5041 -----+-----+-----+-----+-----+-----+-----+  
CGGAGGAGGAGAAGGAGCAGTACAAGTAGATGAGGTAGAAGCCGTACCGGTCTGAAGCGAT  
L L L F L V M F I Y S I F G M A S F A N  
ACGTCGTGGACGAGGCCGGCATCGACGACATGTTCAACTTCAAGACCTTTGGCAACAGCA  
5101 -----+-----+-----+-----+-----+-----+-----+  
TGCAGCACCTGCTCCGGCCGTAGCTGCTGTACAAGTTGAAGTTCTGGAACCGTTGTCGT  
V V D E A G I D D M F N F K T F G N S M  
TGCTGTGCCTGTTCCAGATCACCACCTCGGCCGGCTGGGACGGCCTCCTCAGCCCCATCC  
5161 -----+-----+-----+-----+-----+-----+-----+  
ACGACACGGACAAGGTCTAGTGGTGGAGCCGGCCGACCCTGCCGGAGGAGTCGGGGTAGG  
L C L F Q I T T S A G W D G L L S P I L  
TCAACACGGGGCCCTCCCTACTGCGACCCCAACCTGCCCAACAGCAACGGCTCCCCGGGGGA  
5221 -----+-----+-----+-----+-----+-----+-----+  
AGTTGTGCCCCGGAGGGATGACGCTGGGGTTGGACGGGTGTCTGTTGCCGAGGGCCCCCT  
N T G P P Y C D P N L P N S N G S R G N  
ACTGCGGGAGCCCCGGCGGTGGGCATCATCTTCTTACCACCTACATCATCATCTCCTTCC  
5281 -----+-----+-----+-----+-----+-----+-----+  
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C G S P A V G I I F F T T Y I I I S F L

# Fig. 1a-10

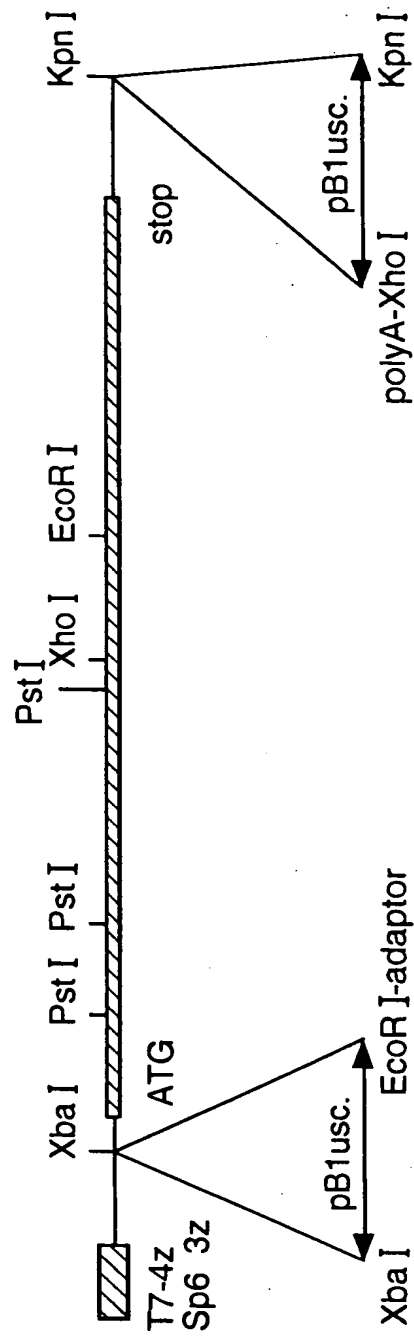
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I V V N M Y I A V I L E N F N V A T E E  
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5401 -----+-----+-----+-----+-----+-----+-----+-----+  
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S T E P L S E D D F D M F Y E T W E K F  
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5461 -----+-----+-----+-----+-----+-----+-----+-----+  
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S G P L R I P K P N Q N I L I Q M D L P  
CGTTGGTCCCCGGGGATAAGATCCACTGTCTGGACATCCTTTTTGCCTTCACAAAGAACG  
5581 -----+-----+-----+-----+-----+-----+-----+-----+  
GCAACCAGGGGCCCTATTCTAGGTGACAGACCTGTAGGAAAAACGGAAGTGTTCCTTGC  
L V P G D K I H C L D I L F A F T K N V  
TCTTGGGAGAATCCGGGGAGTTGGACTCCCTGAAGACCAATATGGAAGAGAAGTTTATGG  
5641 -----+-----+-----+-----+-----+-----+-----+-----+  
AGAACCCTCTTAGGCCCTCAACCTGAGGGACTTCTGGTTATACCTTCTCTTCAAATACC  
L G E S G E L D S L K T N M E E K F M A  
CGACCAATCTCTCCAAAGCATCCTATGAACCAATAGCCACCACCCTCCGGTGGAGCAGG  
5701 -----+-----+-----+-----+-----+-----+-----+-----+  
GCTGGTTAGAGAGGTTTCGTAGGATACTTGGTTATCGGTGGTGGGAGGCCACCTTCGTCC  
T N L S K A S Y E P I A T T L R W K Q E  
AAGACCTCTCAGCCACAGTCATTCAAAGGCCTACCGGAGCTACATGCTGCACCGCTCCT  
5761 -----+-----+-----+-----+-----+-----+-----+-----+  
TTCTGGAGAGTCGGTGTCAAGTMTTCCGGATGGCCTCGATGTACGACGTGGCGAGGA  
D L S A T V I Q K A Y R S Y M L H R S L  
TGACACTCTCCAACACCCTGCATGTGCCCAGGGCTGAGGAGGATGGCGTGTCACTTCCCG  
5821 -----+-----+-----+-----+-----+-----+-----+-----+  
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T L S N T L H V P R A E E D G V S L P G  
GGGAAGGCTACAGTACATTCATGGCAAACAGTGGACTCCCGGACAAATCAGAACTGCCT  
5881 -----+-----+-----+-----+-----+-----+-----+-----+  
CCCTTCCGATGTCATGTAAGTACCGTTTGTCACTGAGGGCCTGTTAGTCTTTGACGGA  
E G Y S T F M A N S G L P D K S E T A S

## Fig. 1a-11

5941 CTGCTACGTCTTTCCCGCCATCCTATGACAGTGTACCAGGGGCCTGAGTGACCGGGCCA  
-----+-----+-----+-----+-----+-----+-----+  
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A T S F P P S Y D S V T R G L S D R A N  
  
6001 ACATTAACCCATCTAGCTCAATGCAAAATGAAGATGAGGTGCTGCTAAGGAAGGAAACA  
-----+-----+-----+-----+-----+-----+-----+  
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I N P S S S M Q N E D E V A A K E G N S  
  
6061 GCCCTGGACCTCAGTGAaggcactcaggcatgcacagggcaggttccaatgtctttctct  
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P G P Q \*  
  
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Fig.1b

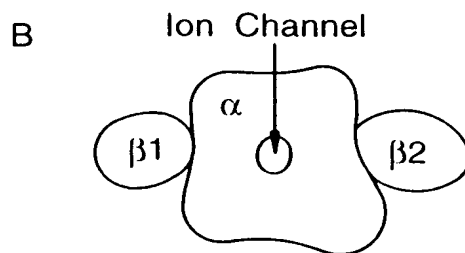
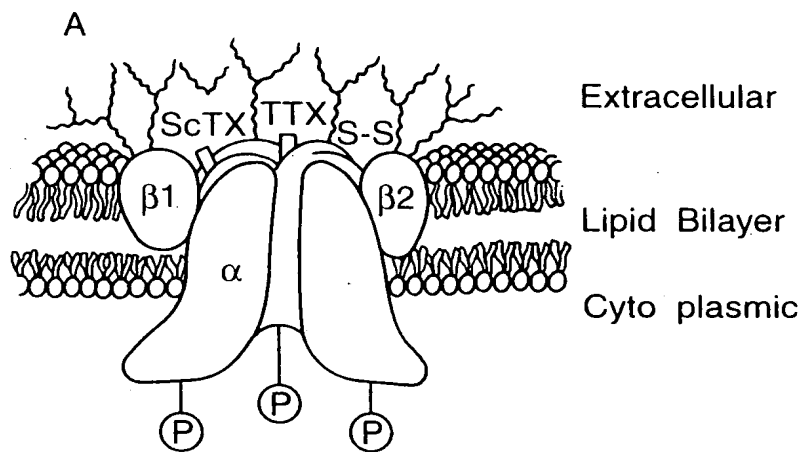
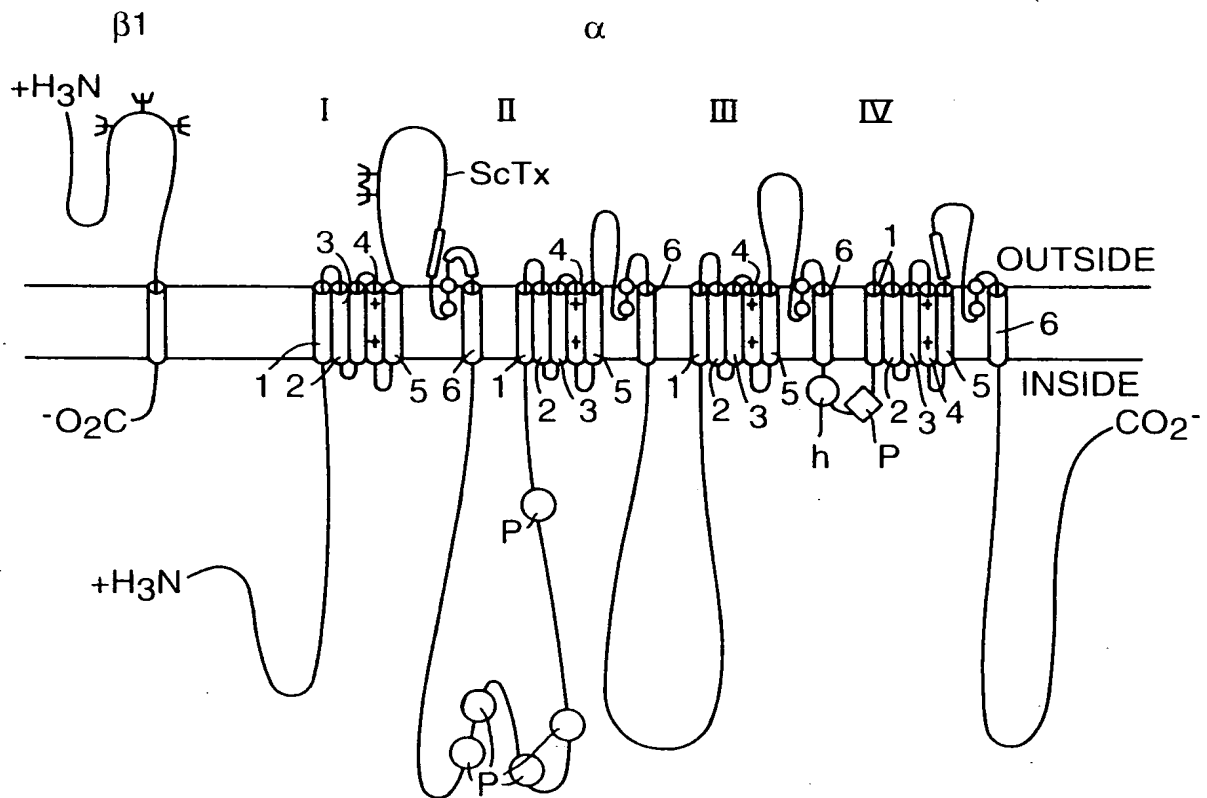
SNS-B voltage gated sodium channel  
PNC IB XOI-construct



Constructs were generated in pGem 3z  
and pGem 4z with bluescript polylinkers

Linearisation site is KPN I

Fig.1c



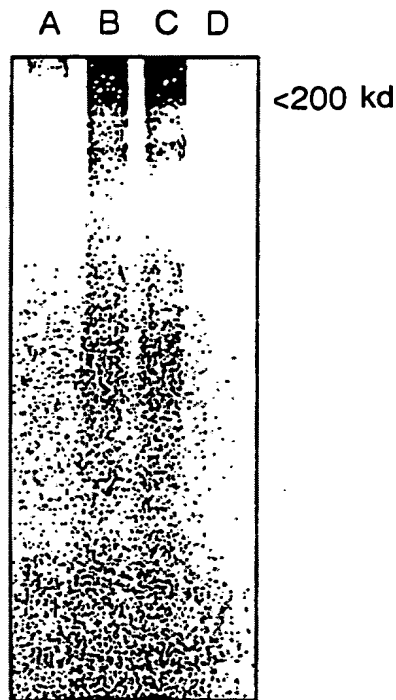
## Fig.2

### Sequence of PCR primers for isolation of human clone probes

- a) *Highly conserved regions of all sodium channels*
- 1) Position 2475-2510 S4 Domain II  
Degenerate primers (20-24mers) encoding amino acid residues RLLRVFKLAKSWPTL or non degenerate primers within this region e.g. 5' gcttgctgcgggtcttcaagc 3'
- 2) Position 3961 - 4010 S4 Domain III  
Degenerate primers encoding the complementary strand encoding residues LRALPLRALS RFEG or non degenerate primers within this region e.g. 5' atcgagacagagcccgagcg 3'
- b) *Unique sequence primers for SNS-homologues*  
e.g. residues with the region 2641-2680  
e.g. 5' acgggtgccgcaaggacggcgtctccgtgtggaacggcgagaag 3'  
and complementary sequence within the region 3375 and 3420  
e.g. 5' ggctatccttcctcttcagctctcaccaggtatggagccaggt 3'

## Fig.3

In vitro synthesis of S-35 methionine labelled SNS-B voltage gated sodium channel in a coupled transcription/translation system



Autoradiograph of a 7.5% SDS polyacrylamide gel, showing the migration of labelled proteins compared to the sizes of known molecular weight markers (Amersham rainbow markers). Lane A control, Lane B SNS-B, Lane C SNS-B, Lane D control. The predicted 200kDa band representing the SNS-B sodium channel is arrowed.

Fig.4a

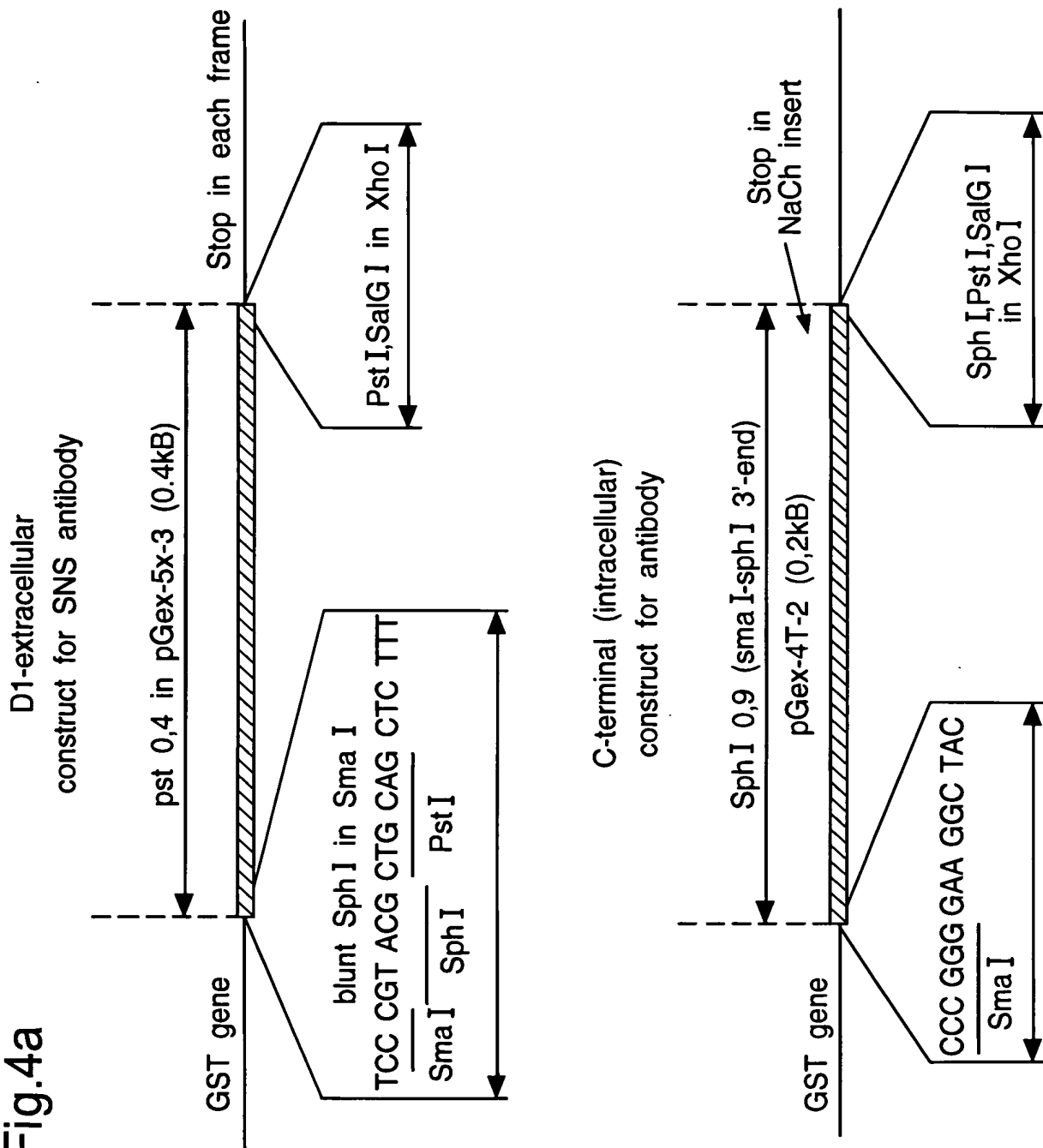




Fig.4b

